PCT10

ENTERED

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   3 <110> APPLICANT: The University of Georgia Research Foundation, Inc
   5 <120> TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
   7 <130> FILE REFERENCE: 235.00210201
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/030,330
C--> 10 <141> CURRENT FILING DATE: 2001-10-19
  12 <150> PRIOR APPLICATION NUMBER: 60/130,436
  13 <151> PRIOR FILING DATE: 1999-04-21
  15 <160> NUMBER OF SEQ ID NOS: 6
  17 <170> SOFTWARE: PatentIn Ver. 2.1
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 843
  21 <212> TYPE: PRT
  22 <213> ORGANISM: Porphyromonas gingivalis
  24 <400> SEQUENCE: 1
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  28 Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
  29               20                  25                  30
  31 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
  32           35                  40                  45
  34 Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
  35       50                  55                  60
  37 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
  38  65                  70                  75                  80
  40 Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
  41               85                  90                  95
  43 Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
  44           100                 105                 110
  46 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
  47           115                 120                 125
  49 Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu
  50     130                 135                 140
  52 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp
  53 145                 150                 155                 160
  55 Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro
  56               165                 170                 175
  58 Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr
  59               180                 185                 190
  61 Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp
  62           195                 200                 205
  64 Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val
  65       210                 215                 220
  67 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met
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RAW SEQUENCE LISTING   DATE: 02/08/2002
PATENT APPLICATION: US/10/030,330   TIME: 11:11:46

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Output Set: N:\CRF3\02082002\J030330.raw

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70 Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala
71               245               250               255
73 Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe
74               260               265               270
76 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu
77               275               280               285
79 Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala
80       290               295               300
82 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala
83 305               310               315                    320
85 Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His
86               325               330               335
88 Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn
89               340               345               350
91 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu
92               355               360               365
94 Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile
95       370               375               380
97 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu
98 385               390               395                    400
100 Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala
101               405               410               415
103 Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn
104               420               425               430
106 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys
107               435               440               445
109 Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser
110       450               455               460
112 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn
113 465               470               475                    480
115 Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr
116               485               490               495
118 Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val
119               500               505               510
121 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr
122       515               520               525
124 Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
125       530               535               540
127 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
128 545               550               555                    560
130 Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
131               565               570               575
133 Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
134               580               585               590
136 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
137               595               600               605
139 Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
140       610               615               620
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RAW SEQUENCE LISTING   DATE: 02/08/2002
PATENT APPLICATION: US/10/030,330   TIME: 11:11:46

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Output Set: N:\CRF3\02082002\J030330.raw

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143 625               630               635               640
145 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
146               645               650               655
148 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
149               660               665               670
151 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val
152       675               680               685
154 Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
155       690               695               700
157 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
158 705               710               715               720
160 Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
161               725               730               735
163 Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
164       740               745               750
166 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
167       755               760               765
169 Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
170       770               775               780
172 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
173 785               790               795               800
175 Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
176               805               810               815
178 Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
179               820               825               830
181 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
182       835               840
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 2532
187 <212> TYPE: DNA
188 <213> ORGANISM: Porphyromonas gingivalis
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192 tctgctccgg ttacgaaaga gcgagctttg agtctggctc ggctggcttt gcgacaggta 120
193 tccttgcgaa tgggacaaac agcagtatct gacaagattt ccatcgatta cgtttatcgg 180
194 caaggagatg ctgagagggg tatcacatca caagaggaag gctctcctgc atattttttat 240
195 gtagctaatc gtggaaataa tgagggctat gctcttgtag cagcagatga cagaataccg 300
196 acaattttag cctattcacc cattggccgt ttcgacatgg acagtatgcc ggacaatctt 360
197 cgcatgtggc tacaaattta cgatcaggaa ataggcctga tactttccgg aaaagctcag 420
198 ctcaatgaag agatattacg taccgagggc gtaccggctg aagtacatgc tctgatggat 480
199 aacggtcatt ttgccaacga tcccatgcga tggaatcaag gttacccatg aacaataag 540
200 gaaccactgc ttcctaatgg caatcatgcc tataccggct gtgttgctac tgctgcagca 600
201 caaatcatgc gctaccatag ctggccgctt caaggtgaag gctctttcga ttatcatgca 660
202 ggttcattag ttggcaactg gtccggcaca tttggtgaaa tgtacgactg gatcaatatg 720
203 cccggaaatc ccgaccttga taatctgact caatctcaag tggatgccta cgccacactg 780
204 atgcgtgatg tgagtgcatc tgtttcgatg agtttttatg aaaatggaag tggtacgtac 840
205 agcgtttatg tagtaggagc cttgcgaaac aactttcgct acaagcgttc actgcagcta 900
206 catgtacgcg ccttatatac ctcacaggag tggcacgata tgatccgcgg ggaacttgcc 960
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207 tccggaaggc cggtctatta tgcagggaat aaccagagca taggacatgc tttcgtttgc 1020
208 gatggttatg cttcggatgg tactttccat ttcaactggg gttggggagg tgtttccaac 1080
209 ggcttctaca aactaacact cctctcgccg acttcgttgg gtatcggagg tgagggaata 1140
210 ggtttttacca tttatcaaga gatcatcacc ggtatcgaac cggctaagac tcccgctgaa 1200
211 gccggtacag atgccttgcc gatcttggca ctgaaagaca tagaagccga gtataaagt 1260
212 gaatccggat tgaacgtagg gtattcgata tataatacag gtgaagagca atcaaatctt 1320
213 gacctcggat acagattgaa caaggctgac ggagaagtca tagaggtgaa aacttcatct 1380
214 atcaatatct cttggtacgg atacggagag catcccgaga gtttctcatt ggcacctaat 1440
215 cagttgtcac aaggaatcaa caccatcacc ctactttatc gtcgcacagg caccgaacag 1500
216 tgggagccgg tacggcatgc acagggagga tatgtcaata gcattaaagt aaatacgaca 1560
217 gacccgaaca atgtcgtagt cacggtagat aataacgaag gcaagctcag tatcgtcccc 1620
218 aacagctttg tcgcagatct gaattcttat gaacatagta cgattacagt acagttcaat 1680
219 agcgacagcc ctgatgagat ccgtacaccc gtagcctttg ctctatctac aggagctact 1740
220 gcggacgatg taatatcttt gggctgggta atggctgaag ttccgggcgg tagcagcaac 1800
221 tatccggtgg tttggtctaa agacgttctc actctctcgg aaggcgacta tacattgtgg 1860
222 tatagatttt ccatcaacaa ccaaaggat gaatggaaaa agatcggaag cgtgtcagta 1920
223 aaaacaccga cagagtatac gcaccccta ttcgaagtgg gccataatca aacttctacc 1980
224 tatacgctgg atatggcaca caacagagta ttgcccgact ttacactcaa aaatctcgga 2040
225 ttgcctttca atggtgagtt ggttgttgtt ttccgccaaa cacaatcctc atcggggtct 2100
226 ttatgggcag ctcaagaaac agtacatatc aagcaaggag aaactttcgt atataaacct 2160
227 gttgtcgaag gccctatacc tgatggatcc tatcgtgcga ccctccatgc attcgtaaac 2220
228 ggacaacaac agttgtacct caaggggaaa aggaactaca cggtgaagat cgtcaatggt 2280
229 acagcggtag aagcaataga atcgtcagaa gagatcagag tattccctaa tccggcacgc 2340
230 gattatgtgg aaatatcggc accttgcatt ccccaagaaa catctatcat tcttttcgat 2400
231 ctgtcaggca agattgtcat gaagaatagt ttatcagcgg ggcatggcag aatggatgtc 2460
232 agccgacttc ctaatggggc ctacatcctt aaggtggatg gatatacgac gaaaataaat 2520
233 atagtgcact aa                                                    2532
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 418
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 3
242 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
243  1               5                  10                  15
245 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
246             20                  25                  30
248 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
249         35                  40                  45
251 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
252     50                  55                  60
254 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
255  65                  70                  75                  80
257 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
258             85                  90                  95
260 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
261             100                 105                 110
263 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
264         115                 120                 125
266 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
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RAW SEQUENCE LISTING   DATE: 02/08/2002
PATENT APPLICATION: US/10/030,330   TIME: 11:11:46

Input Set : A:\sequence.txt.app
Output Set: N:\CRF3\02082002\J030330.raw

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267      130                    135                    140
269 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
270 145                    150                    155                    160
272 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
273                    165                    170                    175
275 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
276                    180                    185                    190
278 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
279            195                    200                    205
281 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
282            210                    215                    220
284 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
285 225                    230                    235                    240
287 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
288                    245                    250                    255
290 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
291                    260                    265                    270
293 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
294            275                    280                    285
296 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
297            290                    295                    300
299 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
300 305                    310                    315                    320
302 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
303                    325                    330                    335
305 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
306                    340                    345                    350
308 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
309            355                    360                    365
311 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
312            370                    375                    380
314 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
315 385                    390                    395                    400
317 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
318                    405                    410                    415
320 Gln Lys
324 <210> SEQ ID NO: 4
325 <211> LENGTH: 15
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 4
330 Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
331   1                    5                    10                    15
334 <210> SEQ ID NO: 5
335 <211> LENGTH: 840
336 <212> TYPE: PRT
337 <213> ORGANISM: Porphyromonas gingivalis
339 <400> SEQUENCE: 5
340 Met Lys Arg Ile Phe Tyr Thr Leu Gly Leu Leu Leu Leu Cys Leu Pro
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/030,330

DATE: 02/08/2002
TIME: 11:11:47

Input Set : **A:\sequence.txt.app**
Output Set: **N:\CRF3\02082002\J030330.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date